



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/603,475
Source: IFW
Date Processed by STIC: 11/6/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>10/602,475</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 ____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 ____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 ____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 ____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 ____ Variable Length	Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 ____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 ____ Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 ____ Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 ____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa , and which residue n or Xaa represents.	
10 ____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 ____ Use of <220>	Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 ____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 ____ Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFWO

RAW SEQUENCE LISTING

DATE: 11/06/2003

PATENT APPLICATION: US/10/602,475

TIME: 09:57:13

Input Set : A:\UF-325XC1.txt

Output Set: N:\CRF4\11062003\J602475.raw

3 <110> APPLICANT: Klee, Harry J.
 4 Lashbrook, Coralie
 5 Shrode, Lori
 7 <120> TITLE OF INVENTION: Materials and Methods for Tissue-Specific Targeting of
 Ethylene

8 Insensitivity in Transgenic Plants
 10 <130> FILE REFERENCE: UF-325XC1
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/602,475
 C--> 12 <141> CURRENT FILING DATE: 2003-06-23

12 <150> PRIOR APPLICATION NUMBER: US 60/390,385

13 <151> PRIOR FILING DATE: 2002-06-21

15 <160> NUMBER OF SEQ ID NOS: 4

17 <170> SOFTWARE: PatentIn version 3.2

19 <210> SEQ ID NO: 1

20 <211> LENGTH: 773

21 <212> TYPE: PRT

22 <213> ORGANISM: Amino acid sequence alignment of ETR2

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27 1 5 10 15

30 Phe Val Ser Pro Val Leu Ala Ile Asn Gly Gly Gly Tyr Pro Arg Cys

31 20 25 30

34 Asn Cys Glu Asp Glu Gly Asn Ser Phe Trp Ser Thr Glu Asn Ile Leu

35 35 40 45

38 Glu Thr Gln Arg Val Ser Asp Phe Leu Ile Ala Val Ala Tyr Phe Ser

39 50 55 60

42 Ile Pro Ile Glu Leu Leu Tyr Phe Val Ser Cys Ser Asn Val Pro Phe

43 65 70 75 80

46 Lys Trp Val Leu Phe Glu Phe Ile Ala Phe Ile Val Leu Cys Gly Met

47 85 90 95

50 Thr His Leu Leu His Gly Trp Thr Tyr Ser Ala His Pro Phe Arg Leu

51 100 105 110

54 Met Met Ala Phe Thr Val Phe Lys Met Leu Thr Ala Leu Val Ser Cys

55 115 120 125

58 Ala Thr Ala Ile Thr Leu Ile Thr Leu Ile Pro Leu Leu Lys Val

59 130 135 140

62 Lys Val Arg Glu Phe Met Leu Lys Lys Lys Ala His Glu Leu Gly Arg

63 145 150 155 160

66 Glu Val Gly Leu Ile Leu Ile Lys Lys Glu Thr Gly Phe His Val Arg

67 165 170 175

70 Met Leu Thr Gln Glu Ile Arg Lys Ser Leu Asp Arg His Thr Ile Leu

71 180 185 190

74 Tyr Thr Thr Leu Val Glu Leu Ser Lys Thr Leu Gly Leu Gln Asn Cys

75 195 200 205

pp 1, 3-4

comple

comply
No Needsee item 10 on Error
Summary
Sheet

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PATENT APPLICATION: US/10/602,475

DATE: 11/06/2003

TIME: 09:57:13

Input Set : A:\UF-325XC1.txt

Output Set: N:\CRF4\11062003\J602475.raw

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78 Ala Val Trp Met Pro Asn Asp Gly Gly Thr Glu Met Asp Leu Thr His
79      210                      215                      220
82 Glu Leu Arg Gly Arg Gly Gly Tyr Gly Gly Cys Ser Val Ser Met Glu
83 225                      230                      235                      240
86 Asp Leu Asp Val Val Arg Ile Arg Glu Ser Asp Glu Val Asn Val Leu
87                      245                      250                      255
90 Ser Val Asp Ser Ser Ile Ala Arg Ala Ser Gly Gly Gly Gly Asp Val
91                      260                      265                      270
94 Ser Glu Ile Gly Ala Val Ala Ala Ile Arg Met Pro Met Leu Arg Val
95                      275                      280                      285
98 Ser Asp Phe Asn Gly Glu Leu Ser Tyr Ala Ile Leu Val Cys Val Leu
99      290                      295                      300
102 Pro Gly Gly Thr Pro Arg Asp Trp Thr Tyr Gln Glu Ile Glu Ile Val
103 305                      310                      315                      320
106 Lys Val Val Ala Asp Gln Val Thr Val Ala Leu Asp His Ala Ala Val
107                      325                      330                      335
110 Leu Glu Glu Ser Gln Leu Met Arg Glu Lys Leu Ala Glu Gln Asn Arg
111                      340                      345                      350
114 Ala Leu Gln Met Ala Lys Arg Asp Ala Leu Arg Ala Ser Gln Ala Arg
115                      355                      360                      365
118 Asn Ala Phe Gln Lys Thr Met Ser Glu Gly Met Arg Arg Pro Met His
119      370                      375                      380
122 Ser Ile Leu Gly Leu Leu Ser Met Ile Gln Asp Glu Lys Leu Ser Asp
123 385                      390                      395                      400
126 Glu Gln Lys Met Ile Val Asp Thr Met Val Lys Thr Gly Asn Val Met
127                      405                      410                      415
130 Ser Asn Leu Val Gly Asp Ser Met Asp Val Pro Asp Gly Arg Phe Gly
131                      420                      425                      430
134 Thr Glu Met Lys Pro Phe Ser Leu His Arg Thr Ile His Glu Ala Ala
135      435                      440                      445
138 Cys Met Ala Arg Cys Leu Cys Leu Cys Asn Gly Ile Arg Phe Leu Val
139      450                      455                      460
142 Asp Ala Glu Lys Ser Leu Pro Asp Asn Val Val Gly Asp Glu Arg Arg
143 465                      470                      475                      480
146 Val Phe Gln Val Ile Leu His Ile Val Gly Ser Leu Val Lys Pro Arg
147                      485                      490                      495
150 Lys Arg Gln Glu Gly Ser Ser Leu Met Phe Lys Val Leu Lys Glu Arg
151                      500                      505                      510
154 Gly Ser Leu Asp Arg Ser Asp His Arg Trp Ala Ala Trp Arg Ser Pro
155      515                      520                      525
158 Ala Ser Ser Ala Asp Gly Asp Val Tyr Ile Arg Phe Glu Met Asn Val
159      530                      535                      540
162 Glu Asn Asp Asp Ser Ser Ser Gln Ser Phe Ala Ser Val Ser Ser Arg
163 545                      550                      555                      560
166 Asp Gln Glu Val Gly Asp Val Arg Phe Ser Gly Gly Tyr Gly Leu Gly
167                      565                      570                      575
170 Gln Asp Leu Ser Phe Gly Val Cys Lys Lys Val Val Gln Leu Ile His
171                      580                      585                      590
174 Gly Asn Ile Ser Val Val Pro Gly Ser Asp Gly Ser Pro Glu Thr Met

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Input Set : A:\UF-325XC1.txt

Output Set: N:\CRF4\11062003\J602475.raw

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175          595          600          605
178 Ser Leu Leu Leu Arg Phe Arg Arg Arg Pro Ser Ile Ser Val His Gly
179          610          615          620
182 Ser Ser Glu Ser Pro Ala Pro Asp His His Ala His Pro His Ser Asn
183 625          630          635          640
186 Ser Leu Leu Arg Gly Leu Gln Val Leu Leu Val Asp Thr Asn Asp Ser
187          645          650          655
190 Asn Arg Ala Val Thr Arg Lys Leu Leu Glu Lys Leu Gly Cys Asp Val
191          660          665          670
194 Thr Ala Val Ser Ser Gly Phe Asp Cys Leu Thr Ala Ile Ala Pro Gly
195          675          680          685
198 Ser Ser Ser Pro Ser Thr Ser Phe Gln Val Val Val Leu Asp Leu Gln
199          690          695          700
202 Met Ala Glu Met Asp Gly Tyr Glu Val Ala Met Arg Ile Arg Ser Arg
203 705          710          715          720
206 Ser Trp Pro Leu Ile Val Ala Thr Thr Val Ser Leu Asp Glu Glu Met
207          725          730          735
210 Trp Asp Lys Cys Ala Gln Ile Gly Ile Asn Gly Val Val Arg Lys Pro
211          740          745          750
214 Val Val Leu Arg Ala Met Glu Ser Glu Leu Arg Arg Val Leu Leu Gln
215          755          760          765
218 Ala Asp Gln Leu Leu
219          770

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222 <210> SEQ ID NO: 2

223 <211> LENGTH: 2893

224 <212> TYPE: DNA

225 <213> ORGANISM: Amino acid sequence alignment of ETR2

227 <400> SEQUENCE: 2

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232 tcagatttgt ctctatctct tcacttttaa gtcttctggt tttgtcatca ccagcttttt      180
234 ttgttctgtc tctgtctttc tctttgtgta tttttattct cgtcatcggt gttcttctat      240
236 gagaggaaga tcggaatgtc gaagagaatt agaagattct cgtacatcac ttcggtggaa      300
238 tttcacaggt cgatgagaga tctgagaact gtttcatttt gatccaaact catctctttc      360
240 agagtataat ggactaagca ttttttttct ccgaagatgg ttaaagaaat agcttcttgg      420
242 ttattgatac tatcaatggt ggtgtttggt tctccggttt tagctataaa cggcgttggt      480
244 tatccacgat gtaactgcga agacgaagga aacagtttct ggagtacaga gaacattcta      540
246 gaaactcaaa gagtaagcga tttcttaate gcagtagctt atttctcaat ccctattgag      600
248 ttactttact tcgtgagttg ttccaatggt ccattcaaat gggttctctt tgagtttata      660
250 gccttcattg ttctttgttg taigactcat ctcttctcat gttggactta ctctgctcat      720
252 ccatttagat taatgatggc gtttactggt ttcaagatgt tgactgcttt agtctcttgt      780
254 gctactgcga ttacgcttat tactttgatt cctctgcttt tgaaagttaa agttagagag      840
256 tttatgctta agaagaaagc tcatgagctt ggtcgtgaag ttggtttgat tttgattaaq      900
258 aaagagactg gctttcatgt tcgtatgctt actcaagaga ttcgtaagtc tttggatcgt      960
260 catacgattc tttatactac tttggttgag ctttcgaaga ctttaggggt gcagaattgt      1020
262 qcggtttgga tgccgaatga cgggtggaac gagatggatt tgactcatga gttgagaggg      1080
264 agaggtggtt atggtggttg ttctgtttct atggaggatt tggatgttgt taggattagg      1140
266 gagagtgatg aagtgaatgt gttgagtgtt gactcgtcca ttgctcgagc tagtggtggt      1200
268 ggtggggatg ttagtgagat tggtgccgtg gctgctatta gaatgccgat gcttcgtggt      1260

```

see den 10 also, this sequence is not an amino acid sequence

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Input Set : A:\UF-325XC1.txt

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270 tcggatttta atggagagct aagttatgcg alacttggtt gtgttttacc gggcgggacg 1320
272 cctcgggatt ggacttatca ggagattgag attglttaaag ttgtggcgga tcaagtaacc 1380
274 gttgcgttag atcatgcagc ggtlcttgaa gagtctcagc ttaigaggga gaagctggcg 1440
276 gaacagaaca gggcgtttgca gatggcgaag agagacgcgt tgagagcgag ccaagcgagg 1500
278 aatgcgtttc agaaaacgat gagcgaaggg atgagggcgt ctatgcattc gatactcggt 1560
280 cttttgtcga tgattcagga cgagaagttg agtgacgagc agaaaatgat tgttgatacg 1620
282 atggttaaaa cagggaaatgt tatgtcgaat ttggtggggg actctatgga tgtgcctgac 1680
284 ggtagatttg gtacggagat gaaaccattt agtctgcata gtacgatcca tgaagcagct 1740
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288 tctctacctg ataattgagt aggtgatgaa agaagggtct ttcaagtgat acttcatata 1860
290 gttggtagtt tagtaaaagcc tagaaaacgt caagaaggat cttcattgat gtttaagggt 1920
292 ttgaaagaaa gaggaagctt ggataggagt gatcatagat gggctgcttg gagatcaccg 1980
294 gcttcttcag cagatggaga tgtgtatata agatttgaaa tgaatgtaga gaatgatgat 2040
296 tcaagttctc aatcatttgc ttctgtttcc tccagagatc aagaagttgg tgatgttaga 2100
298 ttctccggcg gctatgggtt aggacaagat ctaagctttg gtgtttgtaa gaaagtgtg 2160
300 cagttgattc atgggaatat ctcggtgggt cctggctcgg atggttcacc ggagaccatg 2220
302 tcgttgctcc ttcggtttcg acgtagaccc tccatatctg tccatggatc cagcgagtcg 2280
304 ccagctcctg accaccacgc tcaaccacat tcgaattctc tgttacgtgg cttacaagtt 2340
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312 gacggttatg aagtggccat gaggatcagg agtcgatctt ggccgttgat tgtggcgacg 2580
314 acagtgagct tggatgaaga aatgtgggac aagtgtgcac agattggaat caatggagtt 2640
316 gtgagaaagc cagtgtgtgt aagagctatg gagagtgagc tccgaagagt attgttgcaa 2700
318 gctgaccaac ttctctaagt tgttatctca acttctcttc tacattcaaa atttttacac 2760
320 catagattta tgtcaaatat atcaaaatga aatttcgaaa ttgttattat atataccacc 2820
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324 cgaaattgca ttg

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327 <210> SEQ ID NO: 3

328 <211> LENGTH: 2214

329 <212> TYPE: DNA

330 <213> ORGANISM: pLBS107 construct

333 <220> FEATURE:

334 <221> NAME/KEY: CDS

335 <222> LOCATION: (1)..(2214)

337 <400> SEQUENCE: 3

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339 Met Glu Val Cys Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp Glu Leu
340 1 5 10 15
342 tta atg aaa tac caa tac atc tcc gat ttc ttc att gcg att gcg tat 96
343 Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile Ala Tyr
344 20 25 30
346 ttt tcg att cct ctt gag ttg att tac ttt gtg aag aaa tca gcc gtg 144
347 Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val
348 35 40 45
350 ttt ccg tat aga tgg gta ctt gtt cag ttt ggt gct ttt atc gtt ctt 192
351 Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val Leu
352 50 55 60
354 tat gga gca act cat ctt att aac tta tgg act ttc act acg cat tcg 240

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/602,475

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Input Set : A:\UF-325XC1.txt

Output Set: N:\CRF4\11062003\J602475.raw

355	Tyr	Gly	Ala	Thr	His	Leu	Ile	Asn	Leu	Trp	Thr	Phe	Thr	Thr	His	Ser	
356	65					70					75					80	
358	aga	acc	gtg	gcg	ctt	gtg	atg	act	acc	gcg	aag	gtg	tta	acc	gct	gtt	288
359	Arg	Thr	Val	Ala	Leu	Val	Met	Thr	Thr	Ala	Lys	Val	Leu	Thr	Ala	Val	
360					85					90					95		
362	gtc	tcg	tgt	gct	act	gcg	ttg	atg	ctt	gtt	cat	att	att	cct	gat	ctt	336
363	Val	Ser	Cys	Ala	Thr	Ala	Leu	Met	Leu	Val	His	Ile	Ile	Pro	Asp	Leu	
364				100					105					110			
366	ttg	agt	gtt	aag	act	cgg	gag	ctt	ttc	ttg	aaa	aat	aaa	gct	gct	gag	384
367	Leu	Ser	Val	Lys	Thr	Arg	Glu	Leu	Phe	Leu	Lys	Asn	Lys	Ala	Ala	Glu	
368			115					120					125				
370	ctc	gat	aga	gaa	atg	gga	ttg	att	cga	act	cag	gaa	gaa	acc	gga	agg	432
371	Leu	Asp	Arg	Glu	Met	Gly	Leu	Ile	Arg	Thr	Gln	Glu	Glu	Thr	Gly	Arg	
372		130					135					140					
374	cat	gtg	aga	atg	ttg	act	cat	gag	att	aga	agc	act	tta	gat	aga	cat	480
375	His	Val	Arg	Met	Leu	Thr	His	Glu	Ile	Arg	Ser	Thr	Leu	Asp	Arg	His	
376	145				150					155						160	
378	act	att	tta	aag	act	aca	ctt	glt	gag	ctt	ggg	agg	aca	tta	gct	ttg	528
379	Thr	Ile	Leu	Lys	Thr	Thr	Leu	Val	Glu	Leu	Gly	Arg	Thr	Leu	Ala	Leu	
380				165					170						175		
382	gag	gag	tgt	gca	ttg	tgg	atg	cct	act	aga	act	ggg	tta	gag	cta	cag	576
383	Glu	Glu	Cys	Ala	Leu	Trp	Met	Pro	Thr	Arg	Thr	Gly	Leu	Glu	Leu	Gln	
384			180					185					190				
386	ctt	tct	tat	aca	ctt	cgt	cat	caa	cat	ccc	gtg	gag	tat	acg	gtt	cct	624
387	Leu	Ser	Tyr	Thr	Leu	Arg	His	Gln	His	Pro	Val	Glu	Tyr	Thr	Val	Pro	
388			195				200						205				
390	att	caa	tta	ccg	gtg	att	aac	caa	gtg	ttt	ggg	act	agt	agg	gct	gta	672
391	Ile	Gln	Leu	Pro	Val	Ile	Asn	Gln	Val	Phe	Gly	Thr	Ser	Arg	Ala	Val	
392		210				215						220					
394	aaa	ata	tct	cct	aat	tct	cct	gtg	gct	agg	ttg	aga	cct	gtt	tct	ggg	720
395	Lys	Ile	Ser	Pro	Asn	Ser	Pro	Val	Ala	Arg	Leu	Arg	Pro	Val	Ser	Gly	
396	225				230				235						240		
398	aaa	tat	atg	cta	ggg	gag	gtg	gtc	gct	gtg	agg	gtt	ccg	ctt	ctc	cac	768
399	Lys	Tyr	Met	Leu	Gly	Glu	Val	Val	Ala	Val	Arg	Val	Pro	Leu	Leu	His	
400				245					250						255		
402	ctt	tct	aat	ttt	cag	att	aat	gac	tgg	cct	gag	ctt	tca	aca	aag	aga	816
403	Leu	Ser	Asn	Phe	Gln	Ile	Asn	Asp	Trp	Pro	Glu	Leu	Ser	Thr	Lys	Arg	
404			260					265					270				
406	tat	gct	ttg	atg	gtt	ttg	atg	ctt	cct	tca	gat	agt	gca	agg	caa	tgg	864
407	Tyr	Ala	Leu	Met	Val	Leu	Met	Leu	Pro	Ser	Asp	Ser	Ala	Arg	Gln	Trp	
408			275				280						285				
410	cat	gtc	cat	gag	ttg	gaa	ctc	gtt	gaa	gtc	gtc	gct	gat	cag	gtg	gct	912
411	His	Val	His	Glu	Leu	Glu	Leu	Val	Glu	Val	Val	Ala	Asp	Gln	Val	Ala	
412		290				295						300					
414	gta	gct	ctc	tca	cat	gct	gcg	atc	cta	gaa	gag	tcg	atg	cga	gct	agg	960
415	Val	Ala	Leu	Ser	His	Ala	Ala	Ile	Leu	Glu	Glu	Ser	Met	Arg	Ala	Arg	
416	305				310					315					320		
418	gac	ctt	ctc	atg	gag	cag	aat	gtt	gct	ctt	gat	cta	gct	aga	cga	gaa	1008
419	Asp	Leu	Leu	Met	Glu	Gln	Asn	Val	Ala	Leu	Asp	Leu	Ala	Arg	Arg	Glu	

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/602,475

DATE: 11/06/2003

TIME: 09:57:14

Input Set : A:\UF-325XC1.txt

Output Set: N:\CRF4\11062003\J602475.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date